



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Daniell, Henry
- (ii) TITLE OF INVENTION: UNIVERSAL CHLOROPLAST INTEGRATION AND
EXPRESSION VECTORS, TRANSFORMED PLANTS AND PRODUCTS
THEREOF
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: WEISER & ASSOCIATES
 - (B) STREET: 230 South Fifteenth Street, Suite 500
 - (C) CITY: Philadelphia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19102
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/079,640
 - (B) FILING DATE: 15-MAY-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Weiser, Gerard J.
 - (B) REGISTRATION NUMBER: 19,763
 - (C) REFERENCE/DOCKET NUMBER: 922.6588P
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 215-875-8383
 - (B) TELEFAX: 215-875-8394

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Soybean

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTACACACCG CCCGTCACAC TATGGGAGCT GGCCATGCCG AAGTCGTTAC CTTAACCGCA

AGAGGGGGAT	GCCGAAGGCA	GGGCTAGTGA	CTGGAGTGAA	GTCGTAACAA	GGTAGCCGTA	120
CTGGAAGGTG	CGGCTGGATC	ACCTCCTTTT	CAGGGAGAGC	TAATGCTTGT	TGGGTAGTTT	180
AGTTTGACAC	TGCTTCACAC	CCAAAAAGAA	GCGAGTTATG	TCTGAGTCAA	ATTTGGAGAT	240
GGAAGTCTTC	TTTCGTTTCT	CGATGGTGAA	GTAAGACTAA	ACTCATGAGC	TTATTATCCT	300
AGGTCGGAAC	AAGTTGATAG	GAGCTACTTT	TTTCACCCCC	ATATGGGGGT	GAAAAAAGGA	360
AAGAGAGGGA	TGGGGTTTCT	CTTGCTTTTG	GCATAGCGGG	CCCCGGCGGG	AGGCCCCGAC	420
GACGGGCTAT	TAGCTCAGTG	GTAGAGCGCG	CCCCTGATAA	TTGCGTCGTT	GTGCCTGGAC	480
TGTGAGGGCT	CTCAGCCACA	TGGATAGTTT	AATGTGCTCA	TCGGCGCCTG	ACCCTGAGAT	540
GTGGATCATC	CAAGGCACAT	TAGCATGGCG	TACTTCTCCT	GTTTGAACCG	GGGTTTGAAA	600
CCAAACTTAT	CCTCAGGAGG	ATAGATGGGG	CGATTCAAGT	GAGATCCAAT	GTAGATCCAA	660
CTTTCTCTTC	ACTCGTGGGA	TCCGGGCGAT	CCGGGGGGGA	CCACCACGGC	TCCTCTCTTC	720
TCGAGAATTC	ATACATCCCT	TATCAGTATA	TGGACAGTTA	TCTCTCGAGC	ACAGGTTTAG	780
GTTTGGCCTC	AATGGAAAAA	AACGGAGCAC	CTAACAACGT	ATCTTCACAG	ACCAAGAACT	840
ACGAGATCGC	CCCTTTCATT	CTGGGGTGAC	GGTGGGATCG	TACCATTCTGA	GCCTGGGAGC	900
AGGTTTGAAA	AAGGATCTTA	GAGTGTCTAG	GGTTGTGCTA	GGAGGGTCTC	ATAATGCCTT	960
CCTTTTTCTT	CTCATCGGAG	TTATTTCCCA	AAGACTTGCC	ATGGTAAAGA	AGAAGGGGGA	1020
ACAAGCACAC	TTGGAGAGCG	CAGTACAACG	GATAGTTGTA	TGCTGCGTTC	GGGAAGGATG	1080
AATCGCTCCC	GAAAAGGAAT	CTATTGATTC	TCTCCCAATT	GGTTGGAAGT	TAGGTGCGAT	1140
GATTTACTTC	ACGGGCGAGG	TCTCTGGTTC	AAGTCCAAGA	TGGCCCAGCT	GCGTCAAGGA	1200
AAAGAATAGA	AAACTGACTT	GAATCCTTCA	TGCATGCTCC	ACTCGGCTCG	GGGGGATATA	1260
GCTCAGTTGG	TAGAGCTCCG	CTCTTGCAAT	TGGGTCGTTG	CGATTACGGG	TTGGATGTCT	1320
AATTGTCTAG	GCGGTAATGA	TAGTATCTTG	TACCTGAACC	GGTGGCTCAC	TTTTTCTAAG	1380
TAATGGGAAA	GAGGACCGAA	ACATGCCACT	GAAAGACTCT	ACTGAGACAA	AGACGGGCTG	1440
TCAAGAACGT	AGAGGAGGTA	GGATGGGCAG	TTGGTCAGAT	CTAGTATGGA	TCGTACATGG	1500
ACGGTAGTTG	GAGTCGGTGG	CTCTCCTAGG	GTTTCCTCAT	TTGGGATCCT	GGGGAAGAGG	1560
ATCAAGCTGG	CCCTTGCGAA	CAGCTTGATG	CACTATCTCC	CTTCAACCCT	TTGAGCGAAA	1620
TGTGGCAAAA	GGAAAAAGAA	TCCATGGACC	GACCCCATCG	TCTCCACCCC	GTAGGAACCTA	1680
CGAGATCACC	CCAAGGAACG	CCTTCGGCAT	CCAGGGGTCG	CGGACCGACC	ATAGAACCCT	1740
GTTCAAAAAG	CGGAACGCAT	TAGCTATCCG	CTCTCAGGTT	GGACAGTAAG	GGTCGGAGAA	1800
GGGCAATCAC	TCATTCTTAG	TTAGAATGGG	ATTCCAACCTC	AGCACCTTTT	GAGATTTTGA	1860
GAAGAGTTGC	TCTTTGGAGA	GCACAGTACG	ATGAAAGTTG	TGAGCTGTGT	TCGGGGGGGA	1920

GTTATTGTCT ATCGTTGGCC TCTATGGTAG AATCAGTCGG GGCCTGAGAG GCGGTGGTTT 1980
 ACCCTGTGGC GGATGTCAGC GGTTCGAGTC CGCTTATCTC CAACTCGTGA ACTTAGTCGA 2040
 TACAAAGCTA 2050

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tobacco

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTACACACCG CCCGTCACAC TATGGGAGCT GGCCATGCCC GAAGTCGTTA CCTTAACCGC 60
 AAGGAGGGGG ATGCCGAAGG CAGGGCTAGT GACTGGAGTG AAGTCGTAAC AAGGTAGCCG 120
 TACTGGAAGG TGCGGCTGGA TCACCTCCTT TTCAGGGAGA GCTAATGCTT GTTGGGTATT 180
 TTGGTTTGAC ACTGCTTCAC ACCCCCCAAA AAAAGAAGGG AGCTACGTCT GAGTTAAACT 240
 TGGAGATGGA AGTCTTCTTT CCTTTCTCGA CGGTGAAGTA AGACCAGCTC ATGAGCTTAT 300
 TATCCTAGGT CGGAACAAGT TGATAGGACC CCCTTTTTTA CGTCCCCATG TTCCCCCCGT 360
 GTGGCGACAT GGGGCGAAAA AAGGAAAGAG AGGGATGGGG TTTCTCTCGC TTTTGGCATA 420
 GCGGGCCCCC AGTGGGAGGC TCGCACGACG GGCTATTAGC TCAGTGGTAG AGCGCGCCCC 480
 TGATAATTGC GTCGTTGTGC CTGGGCTGTG AGGGCCTCTC AGCCACATGG ATAGTTCAAT 540
 GTGCTCATCG GCGCCTGACC CTGAGATGTG GATCATCCAA GGCACATTAG CATGGCGTAC 600
 TCCTCCTGTT CGAACCGGGG TTTGAAACCA AACTCCTCCT CAGGAGGATA GATGGGGCGA 660
 TTCGGGTGAG ATCCAATGTA GATCCAACCT TCGATTCACT CGTGGGATCC GGGCGGTCCG 720
 GGGGGACCAC CACGGCTCCT CTCTTCTCGA GAATCCATAC ATCCCTTATC AGTGATGGA 780
 CAGCTATCTC TCGAGCACAG GTTTAGCAAT GGGAAAATAA AATGGAGCAC CTAACAACGC 840
 ATCTTCACAG ACCAAGAACT ACGAGATCGC CCCTTTCATT CTGGGGTGAC GGAGGGATCG 900
 TACCATTCTGA GCCGTTTTTT TCTTGA CTGAAATGAGC AGGTTTGAAA AAGGATCTTA 960
 GAGTGTCTAG GGTGGGCCA GGAGGGTCTC TTAACGCCCT CTTTTTCTT CTCATCGGAG 1020
 TTATTTTACA AAGACTTGCC AGGGTAAGGA AGAAGGGGGG AACAAGCACA CTTGGAGAGC 1080
 GCAGTACAAC GGAGAGTTGT ATGCTGCGTT CGGGAAGGAT GAATCGCTCC CGAAAAGGAA 1140

TCTATTGATT CTCTCCCAAT TGGTTGGACC GTAGGTGCGA TGATTTACTT CACGGGCGAG	1200
GTCTCTGGTT CAAGTCCAGG ATGGCCCAGC TGCGCCAGGG AAAAGAATAG AAGAAGCATC	1260
TGACTACTTC ATGCATGCTC CACTTGGCTC GGGGGGATAT AGCTCAGTTG GTAGAGCTCC	1320
GCTCTTGCAA TTGGGTCGTT GCGATTACGG GTTGATGTC TAATTGTCCA GCGGGTAATG	1380
ATAGTATCTT GTACCTGAAC CGGTGGCTCA CTTTTTCTAA GTAATGGGGA AGAGGACCGA	1440
AACGTGCCAC TGAAAGACTC TACTGAGACA AAGATGGGCT GTCAAGAACG TAGAGGAGGT	1500
AGGATGGGCA GTTGGTCAGA TCTAGTATGG ATCGTACATG GACGGTAGTT GGAGTCGGCG	1560
GCTCTCCCAG GGTTCCTCA TCTGAGATCT CTGGGGAAGA GGATCAAGTT GGCCCTTGCG	1620
AACAGCTTGA TGCATATCT CCCTTCAACC CTTTGAGCGA AATGCGGCAA AAGAAAAGGA	1680
AGGAAAATCC ATGGACCGAC CCCATCATCT CCACCCGTA GGAACCTACGA GATCACCCCA	1740
AGGAACGCCT TCGGCATCCA GGGGTCACGG ACCGACCATA GAACCCTGTT CAATAAGTGG	1800
AACGCATTAG CTGTCCGCTC TCAGGTTGGG CAGTCAGGGT CGGAGAAGGG CAATGACTCA	1860
TTCTTAGTTA GAATGGGATT CCAACTCAGC ACCTTTTGAG TGAGATTTTG AGAAGAGTTG	1920
CTCTTTGGAG AGCACAGTAC GATGAAAGTT GTAAGCTGTG TTCGGGGGGG AGTTATTGTC	1980
TATCGTTGGC CTCTATGGTA GAATCAGTCG GGGGACCTGA GAGGCGGTGG TTTACCCTGC	2040
GGCGGATGTC AGCGGTTCTGA GTCCGCTTAT CTCCAACCTCG TGAACCTAGC CGATACAAAG	2100
CTT	2103

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Maize

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTACACACCG CCCGTCACAC TATAGGAGCT GGCCAGGTTT GAAGTCATTA CCCTTAACCG	60
TAAGGAGGGG GATGCCTAAG GCTAGGCTTG CGACTGGAGT GAAGTCGTAA CAAGGTAGCC	120
GTACTGGAAG GTGCGGCTGG ATCACCTCCT TTTCAGGGAG AGCTAAGTCT TATGCTTATT	180
GGGTATTTTG GTTTGACACT GCTTCACGCC CAAAAGAAG GCAGCTACGT CTGAGCTAAA	240
CTTGGATATG GAAGTCTTCT TTCGTTTAGG GTGAAGTAAG ACCAAGCTCA TGAGCTTATT	300

ATCCTAGGTC	GGAACAAATT	AGTTGATAGT	GATAGGATCC	CCTTTTTGAC	GTCCCCATGT	360
CCCCCGTGT	GGCGGCATGG	GGATGTCAAA	AGGAAAGGGA	TGGAGTTTTT	CTCGCTTTTG	420
GCGTAGCGGC	CTCCCTTTGG	GAGGCCGCGC	GACGGGCTAT	TAGCTCAGTG	GTAGAGCGCG	480
CCCCTGATAA	TTCGTCGTTG	TGCCTCGGCT	GTGAGGGCTC	TCAGCCACAT	GGATAGTTCA	540
ATGTGCTCAT	CAGCGCCTGA	CCCGAAGATG	TGGATCATCC	AAGGCACATT	AGCATGGCGT	600
ACTCCTCCTG	TTTGAATCGG	AGTTTGAAAC	CAAACAACT	TCTCCTCAGG	AGGATAGATG	660
GGGCGATTCA	GGTGAGATCC	CATGTAGATC	GAACTTTCTA	TTCACTCGTG	GGATCCGGGC	720
GGTCCGGGGG	GGGGCCACCG	GGGCTCCTCT	CTTCTCGAGA	ATCCATACAT	CCCTTATCAG	780
TGTATGGAGA	GCTATCTCTC	GAGCACAGGT	TGAGGTTTCGT	CCTCAATGGG	AAAATGGAGC	840
ACCTAACAAAC	GCATCTTCAC	AGACCAAGAA	CTACGAGATC	ACCCCTTTCA	TTCTGGGGTG	900
ACGGAGGGAT	CGTACCATTG	GAGCCCTTGA	CTCGAAATGG	GAGCAGAGCA	GGTTTGAAAA	960
AGGATCTTAG	AGTGTCTAGG	GTTGGGCCAG	GAGGGTCTCT	TAACCCCTTC	TTTTTTCTGC	1020
CCATCGGAGT	TATTTCCCAA	GGACTTGCCG	TGGTAAGGGG	GAGAAGGGGG	AAGAAGCACA	1080
CTTGAAGAGC	GCAGTACAAC	GGGAGTTGT	ATGCTGCGTT	CGGGAAGGAT	GGATCGCTCC	1140
CGAAAAGGAG	TCTATTGATT	CTCTCCCAAT	TGGTTGGATC	GTAGGGGCGA	TGATTTACTT	1200
CACGGGCGAG	GTCTCTGGTT	CAAGTCCAGG	ATGGCCCAGC	TGCGCAGGGA	AAAGAATAGA	1260
AGAAGCATCT	GA CTCTTTCA	TGCATACTCC	ACTTGGCTCG	GGGGGGATAT	AGCTCAGTTG	1320
GTAGAGCTCC	GCTCTTGCAA	TTGGGTCGTT	GCGATTACGG	GTTGGCTGTC	TAATTGTCCA	1380
GGCGGTAATG	ATAGTATCTT	GTACCTGAAC	CGGTGGCTCA	CTTTTTCTAA	GTAATGGGGA	1440
AGAGGACTGA	AACATGCCAC	TGAAAGACTC	TACTGAGACA	AAAAGATGGG	CTGTCAAAAA	1500
GGTAGAGGAG	GTAGGATGGG	CAGTTGGTCA	GATCTAGTAT	GGATCGTACA	TGGACGATAG	1560
TTGGAGTCGG	CGGCTCTCCT	AGGCTTCCCT	CATCTGGGAT	CCCTGGGGAA	GAGGATCAAG	1620
TTGGCCCTTG	CGAATAGCTT	GATGCACTAT	CTCCCTTCAA	CCCTTTGAGC	GAAATGTGGC	1680
AAAAGGAAGG	AAAATCCATG	GACCGACCCC	ATTGTCTCCA	CCCCGTAGGA	ACTACGAGAT	1740
CACCCCAAGG	AGTTCGTCCT	CAATGGGGGT	CTATCGGACC	GACCATAGAT	CCTGTTCAAT	1800
AAGTGGAACA	CAATAGCCGT	CCGCTCTCCG	GTTGGGCAGT	AAGGGTCGGA	GGAGGGCAAT	1860
CACTCGTTCT	TATTAGAATG	GGATTCCAAC	TCAGCACCTT	TTGTTTTGGG	ATTTTGAGAA	1920
GAGTTGCTCT	TTGGAGAGCA	CAGTACGATG	AAAGTTGTAA	GCTGTGTTTCG	GGGGGGAGTT	1980
ATTGCCTATC	GTTGTCTCTT	ATGGTAGAAC	CCGTCGGGGA	GGCCTGAGAG	GCGGTGGTTT	2040
ACCCTGTGGC	GGATGTCAGC	GGTTCGAGTC	CGCTTATCTC	CAGCCCGTGA	ACTTAGCGGA	2100

TAC

2103

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Epifagus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGCGCTAG GAAAAAATA TAAAAAGCAT CTGATTACTT CATGCATGCT

50

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tobacco

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTGCGCCAG GGAAAAGAAT AGAAGAAGCA TCTGACTACT TCATGCATGC TCCACTTGGC

60

TCGG

64

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helianthus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGTGCGCCAG GGAAAAGAAT AGAAGAAGCG TCTGACTCCT TCATGCATGC TCCACTTGGC

60

TCGG

64

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Oenothera

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTGCGCAAA GGAAAAGAAT AGAAGAAGCA TCTGACTCCT TCATGCATGC TCCACTTGGC 60

TCGG 64

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Alnus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTGCGCCAA GTAAAAGAAT AGAAGAAGCA TCTGACTCCT TCATGCATGC TCCACTTGGC 60

TCGG 64

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rice

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGCGCCAG GGAAAAGAAT AGAAGAAGCA TCTGACTCTT TCATGCATAC TCCACTTGGC 60
TCGG 64

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Maize

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTGCGCAGG GAAAAGAATA GAAGAAGCAT CTGACTCTTT CATGCATACT CCACTTGGCT 60
CGG 63

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Soybean

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTGCGTCAA GGAAAAGAAT AGAAAAGTGA CTTGACTCCT TCATGCATGC TCCACTCGGC 60
TCGG 64

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Pea

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTGCGCCAA GGAAAAGACT AAAAGACGGA TTTGACTCCT TCATGCATGC TCCAACTTGG 60
CTCGG 65

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Spinach

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTGCGCCAA GAATAAGAAT CGAAGAAGCG TCTGACTCCT TCATGCATGC TCCACTTGGC 60
TCGG 64

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCCAGGGAA 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Tobacco

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGAGCCAAG TGGAGCATGC ATGAAGTAGT CAGATGCTTC TTCTATTCTT TTCCCTGGCG 60
 CAGC 64

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Cuscuta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCGAGCCAAG TGGAGCATGC ATGAAGTAGT CAGATACTTC TTCGATTCTT TTCCCTGGCG 60
 CAGC 64

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Val Gly Val Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val Pro Gly Val Pro
 1 5